

SEQUENCE LISTING

<110> Presnell, Scott R.
 Xu, Wenfeng
 Kindsvogel, Wayne
 Chen, Zhi

<120> Human Cytokine Receptor

<130> 99-93

<150> US 60/169,049

<151> 1999-12-03

<150> US 60/232,219

<151> 2000-09-13

<150> US 60/244,610

<151> 2000-10-31

<160> 36

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(693)

<400> 1

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | atg | cct | aaa | cat | tgc | ttt | cta | ggc | ttc | ctc | atc | agt | ttc | ttc | ctt | 48 |
| Met | Met | Pro | Lys | His | Cys | Phe | Leu | Gly | Phe | Leu | Ile | Ser | Phe | Phe | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| act | ggg | gta | gca | gga | act | cag | tca | acg | cat | gag | tct | ctg | aag | cct | cag | 96 |
| Thr | Gly | Val | Ala | Gly | Thr | Gln | Ser | Thr | His | Glu | Ser | Leu | Lys | Pro | Gln | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |

| | |
|---|-----|
| agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag | 144 |
| Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln | |
| 35 40 45 | |
| cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac | 192 |
| Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr | |
| 50 55 60 | |
| aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt | 240 |
| Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly | |
| 65 70 75 80 | |
| act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag | 288 |
| Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln | |
| 85 90 95 | |
| gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca | 336 |
| Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser | |
| 100 105 110 | |
| gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata | 384 |
| Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile | |
| 115 120 125 | |
| gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta | 432 |
| Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val | |
| 130 135 140 | |
| att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat | 480 |
| Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn | |
| 145 150 155 160 | |
| gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att | 528 |
| Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile | |
| 165 170 175 | |
| aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga | 576 |
| Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg | |
| 180 185 190 | |
| gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg | 624 |
| Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val | |
| 195 200 205 | |

gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa 672
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

gag aga tgt gtg gaa att cca tgacttgtgg aatttggcat tcagcaatgt 723
 Glu Arg Cys Val Glu Ile Pro
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtggt tgaaggatct tatttaaaat 783
 tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843
 ccattctttt atcctttata tttcatttta aactatattt gaacgacatt ccccccgaat 903
 aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttattt 963
 ctgaatgtaa catccctaata aacaaccttc atttcttcta tacagcaaaa taaaaattta 1023
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 caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgtctt 1863
 tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923
 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagt ataaatggat 1983
 taaaaaatat tcagaaatgt attgggggt ggaggagaat aagaggcaga gcaagagcta 2043
 gagaattggt ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca 2103
 gagactgaaa aaaaaaaaaat gctcgagcgg ccgccatata cttggt 2149

<210> 2

<211> 231

<212> PRT

<213> Homo sapiens

<400> 2

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15

<210> 3
<211> 693
<212> DNA
<213> Artificial Sequence

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

$\langle 223 \rangle$ n = A, T, C or G

<400> 3

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| atgatgccna | arcaytgytt | yytnggntty | ytnathwsnt | tyttyytnac | ngngngtngcn | 60 |
| ggnacncarw | snacncayga | rwsnythaar | ccncarmgng | tncarttyca | rwsnmgnaay | 120 |
| ttycayaaya | thytncartg | gcarccnggn | mgngchnytna | cnggnaayws | nwsngtntay | 180 |
| ttygtncart | ayaarathta | yggncarmgn | cartggaara | ayaargarga | ytgytggggg | 240 |
| acncargary | tnwsntgyga | yytnacnwsn | garacnwsng | ayathcarga | rccntaytay | 300 |
| ggnmgngtnm | gngcngcnws | ngcnggnwsn | taywsngart | ggwsnatgac | nccnmgntty | 360 |
| acnccntggt | gggaracnaa | rathgayccn | ccngtnatga | ayathacna | rgtnaayggg | 420 |
| wsnytnytn | tnathytnca | ygcnccnaay | ytnccntaym | gntaycaraa | rgaraaraay | 480 |
| gtwnsnathg | argaytayta | ygarytnytn | taymgngtnt | tyathathaa | yaaywsnytn | 540 |
| garaargarc | araargtnta | ygarggngcn | caymgngcng | tngarathga | rgcnytnacn | 600 |
| ccncaywsnw | sntaytgygt | ngtngcngar | athtaycarc | cnatgytnga | ymgnmgngwsn | 660 |
| carmgnwsng | argarmgntg | ygtngarath | ccn | | | 693 |

<210> 4
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220> .
 <223> Peptide linker.

<400> 4
 Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 5
 <211> 699
 <212> DNA
 <213> Homo sapiens

| | |
|-------------|---|
| <400> 5 | |
| gagcccagat | cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag 60 |
| ggggcaccgt | cagtcttcct cttcccccca aaaccaaggg acaccctcat gatctcccgg 120 |
| acccttgagg | tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180 |
| aactggtacg | tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 240 |
| tacaacagca | cgtaccgtgt ggtcagcgct ctcaccgtcc tgcaccagga ctggctgaat 300 |
| ggcaaggagt | acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360 |
| atctccaaaag | ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420 |
| gatgagctga | ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480 |
| gacatcgccg | tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540 |
| cccgtgctgg | actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 600 |
| aggtggcagc | aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660 |
| tacacgcaga | agagcctctc cctgtctccg ggtaaataa 699 |

<210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC29181

<400> 6
 gcggatccac tcagtcaacg catgagtctc tg 32

<210> 7
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC29182

<400> 7
 gcagatcttg gaatttccac acatctctct tca 33

<210> 8
 <211> 108
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(108)

<400> 8
 atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc 48
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15

gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc 96
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30

ttc cgt aga tcc 108

Phe Arg Arg Ser
35

<210> 9
<211> 36
<212> PRT
<213> Homo sapiens

<400> 9
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
20 25 30

Phe Arg Arg Ser
35

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu (CEE) Tag amino acid sequence

<400> 10
Glu Tyr Met Pro Met Glu
1 5

<210> 11
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG Tag amino acid sequence

<400> 11
Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 12
<211> 6
<212> PRT

001021163460

<213> Artificial Sequence

<220>

<223> His Tag amino acid sequence

<400> 12

His His His His His His
1 5

<210> 13

<211> 210

<212> PRT

<213> Homo sapiens

<400> 13

Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln Arg Val Gln Phe Gln
1 5 10 15
Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln Pro Gly Arg Ala Leu
20 25 30
Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr Lys Ile Tyr Gly Gln
35 40 45
Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly Thr Gln Glu Leu Ser
50 55 60
Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln Glu Pro Tyr Tyr Gly
65 70 75 80
Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser Glu Trp Ser Met Thr
85 90 95
Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile Asp Pro Pro Val Met
100 105 110
Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val Ile Leu His Ala Pro
115 120 125
Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn Val Ser Ile Glu Asp
130 135 140
Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile Asn Asn Ser Leu Glu
145 150 155 160
Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg Ala Val Glu Ile Glu
165 170 175
Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val Ala Glu Ile Tyr Gln
180 185 190
Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu Glu Arg Cys Val Glu
195 200 205
Ile Pro
210

09728941.120100

<210> 14
 <211> 1116
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (21)...(557)

<400> 14

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| tcgagttaga attgtctgca atg gcc gcc ctg cag aaa tct gtg agc tct ttc | 53 |
| Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe | |
| 1 5 10 | |
| ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg | 101 |
| Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu | |
| 15 20 25 | |
| gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac | 149 |
| Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp | |
| 30 35 40 | |
| aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg | 197 |
| Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu | |
| 45 50 55 | |
| gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att | 245 |
| Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile | |
| 60 65 70 75 | |
| ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg | 293 |
| Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu | |
| 80 85 90 | |
| atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa | 341 |
| Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln | |
| 95 100 105 | |
| tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc | 389 |
| Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala | |
| 110 115 120 | |

09732941.120100

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
 Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
 125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
 140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
 160 165 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587
 Met Ser Leu Arg Asn Ala Cys Ile
 175

taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
 aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
 tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag 767
 catagatatt tattgataac atttcattgt aactggtggt ctatacacag aaaacaattt 827
 attttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
 aaacccttaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat 947
 tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa 1007
 acatcattcg atattgctac ttgagtgtaa ggctaataat gatatttatg acaataatta 1067
 tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta 1116

<210> 15

<211> 179

<212> PRT

<213> Homo sapiens

<400> 15

Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
 1 5 10 15
 Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
 20 25 30
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80

His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC25963

<400> 16

agtcaacgca tgagtctctg aag

23

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28354

<400> 17

accaacaaag agccattgac ttg

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<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC21195

<400> 18
gaggagacca taacccccga cag 23

<210> 19
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<223> Oligonucleotide primer ZC21196

<400> 19
catagctccc accacacgat ttt 23

<210> 20
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<223> Oligonucleotide primer ZC14063

<400> 20
caccagacat aatagctgac agact 25

<210> 21
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<223> Oligonucleotide primer ZC17574

<400> 21
ggtrttgctc agcatgcaca c 21

<210> 22
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<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC17600

<400> 22

catgtaggcc atgaggtcca ccac

24

<210> 23

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC27659

<400> 23

tcaagctgag ttctctgtat gg

22

<210> 24

<211> 2831

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (34)...(1755)

<400> 24

tagaggccaa gggagggctc tgtgccagcc ccg atg agg acg ctg ctg acc atc
Met Arg Thr Leu Leu Thr Ile
1 5

54

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
10 15 20

102

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
25 30 35

150

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
40 45 50 55

198

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt

246

09700911100100

| | |
|---|-----|
| Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys | |
| 60 65 70 | |
| cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac | 294 |
| Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn | |
| 75 80 85 | |
| ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc | 342 |
| Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly | |
| 90 95 100 | |
| cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act | 390 |
| Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr | |
| 105 110 115 | |
| acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att | 438 |
| Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile | |
| 120 125 130 135 | |
| cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc | 486 |
| Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly | |
| 140 145 150 | |
| cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta | 534 |
| His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu | |
| 155 160 165 | |
| gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag | 582 |
| Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln | |
| 170 175 180 | |
| aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc | 630 |
| Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly | |
| 185 190 195 | |
| acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac | 678 |
| Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr | |
| 200 205 210 215 | |
| atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc | 726 |
| Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe | |
| 220 225 230 | |

001021-11682460

| | |
|---|------|
| tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc | 774 |
| Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys | |
| 235 240 245 | |
| tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc | 822 |
| Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser | |
| 250 255 260 | |
| ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag | 870 |
| Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln | |
| 265 270 275 | |
| gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg | 918 |
| Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu | |
| 280 285 290 295 | |
| gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag | 966 |
| Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu | |
| 300 305 310 | |
| ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta | 1014 |
| Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu | |
| 315 320 325 | |
| ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc | 1062 |
| Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro | |
| 330 335 340 | |
| cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc | 1110 |
| Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val | |
| 345 350 355 | |
| ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca | 1158 |
| Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro | |
| 360 365 370 375 | |
| ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc | 1206 |
| Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala | |
| 380 385 390 | |
| cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg | 1254 |
| Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met | |
| 395 400 405 | |

| | | | | | | | | | | | | | | | | | | | | |
|---|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|-----|--|--|-----|
| gaa Glu | ggt Gly | tct Ser | ggc Gly | aaa Lys | gac Asp | tcc Ser | ccc Pro | act Thr | ggg Gly | aca Thr | ctt Leu | tct Ser | agt Ser | cct Pro | aaa Lys | 1302 | | | | |
| 410 | | | | | | | | | | | | | | | | 415 | 420 | | | |
| cac His | ctt Leu | agg Arg | cct Pro | aaa Lys | ggt Gly | cag Gln | ctt Leu | cag Gln | aaa Lys | gag Glu | cca Pro | cca Pro | gct Ala | gga Gly | agc Ser | 1350 | | | | |
| 425 | | | | | | | | | | | | | | | | 430 | 435 | | | |
| tgc Cys | atg Met | tta Leu | ggt Gly | ggc Gly | ctt Leu | tct Ser | ctg Leu | cag Gln | gag Glu | gtg Val | acc Thr | tcc Ser | ttg Leu | gct Ala | atg Met | 1398 | | | | |
| 440 | | | | | | | | | | | | | | | | 445 | 450 | | | 455 |
| gag Glu | gaa Glu | tcc Ser | caa Gln | gaa Glu | gca Ala | aaa Lys | tca Ser | ttg Leu | cac His | cag Gln | ccc Pro | ctg Leu | ggg Gly | att Ile | tgc Cys | 1446 | | | | |
| 460 | | | | | | | | | | | | | | | | 465 | 470 | | | |
| aca Thr | gac Asp | aga Arg | aca Thr | tct Ser | gac Asp | cca Pro | aat Asn | gtg Val | cta Leu | cac His | agt Ser | ggg Gly | gag Glu | gaa Glu | ggg Gly | 1494 | | | | |
| 475 | | | | | | | | | | | | | | | | 480 | 485 | | | |
| aca Thr | cca Pro | cag Gln | tac Tyr | cta Leu | aag Lys | ggc Gly | cag Gln | ctc Leu | ccc Pro | ctc Leu | ctc Leu | tcc Ser | tca Ser | gtc Val | cag Gln | 1542 | | | | |
| 490 | | | | | | | | | | | | | | | | 495 | 500 | | | |
| atc Ile | gag Glu | ggc Gly | cac His | ccc Pro | atg Met | tcc Ser | ctc Leu | cct Pro | ttg Leu | caa Gln | cct Pro | cct Pro | tcc Ser | ggt Gly | cca Pro | 1590 | | | | |
| 505 | | | | | | | | | | | | | | | | 510 | 515 | | | |
| tgt Cys | tcc Ser | ccc Pro | tcg Ser | gac Asp | caa Gln | ggt Gly | cca Pro | agt Ser | ccc Pro | tgg Trp | ggc Gly | ctg Leu | ctg Leu | gag Glu | tcc Ser | 1638 | | | | |
| 520 | | | | | | | | | | | | | | | | 525 | 530 | | | 535 |
| ctt Leu | gtg Val | tgt Cys | ccc Pro | aag Lys | gat Asp | gaa Glu | gcc Ala | aag Lys | agc Ser | cca Pro | gcc Ala | cct Pro | gag Glu | acc Thr | tca Ser | 1686 | | | | |
| 540 | | | | | | | | | | | | | | | | 545 | 550 | | | |
| gac Asp | ctg Leu | gag Glu | cag Gln | ccc Pro | aca Thr | gaa Glu | ctg Leu | gat Asp | tct Ser | ctt Leu | ttc Phe | aga Arg | ggc Gly | ctg Leu | gcc Ala | 1734 | | | | |
| 555 | | | | | | | | | | | | | | | | 560 | 565 | | | |
| ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tgggtgcttcc | | | | | | | | | | | | | | | | 1785 | | | | |

Leu Thr Val Gln Trp Glu Ser
570

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tccctgtccc taccagtggt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca 1845
cactctgcga tctggcctca gacgggtgcc cttgagagaa gcagagggag tggcatgcag 1905
ggcccctgcc atgggtgcgc tcctcaccgg aacaaagcag catgataagg actgcagcgg 1965
gggagctctg gggagcagct tgtgtagaca agcgcgtgct cgctgagccc tgcaaggcag 2025
aaatgacagt gcaaggagga aatgcagga aactcccgag gtccagagcc ccacctccta 2085
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Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35           40           45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50           55           60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65           70           75           80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
 85           90           95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
100           105           110

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007894.120100

Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
 225 230 235 240
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
 245 250 255
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
 260 265 270
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
 275 280 285
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
 290 295 300
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
 305 310 315 320
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
 325 330 335
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
 340 345 350
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
 355 360 365
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
 370 375 380
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
 385 390 395 400
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
 405 410 415
 Gly Thr Leu Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
 420 425 430
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445

007027 1120100

Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
 530 535 540
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
 545 550 555 560
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
 565 570

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27

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36

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<223> Oligonucleotide primer ZC25964

<400> 31

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23

<210> 32

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<223> Oligonucleotide primer ZC14666

<400> 32

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18

<210> 33

<211> 22

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<400> 33

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22

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<211> 211

<212> PRT

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| Pro | Glu | Asp | Pro | Ser | Asp | Leu | Leu | Gln | His | Val | Lys | Phe | Gln | Ser | Ser |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Asn | Phe | Glu | Asn | Ile | Leu | Thr | Trp | Asp | Ser | Gly | Pro | Glu | Gly | Thr | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asp | Thr | Val | Tyr | Ser | Ile | Glu | Tyr | Lys | Thr | Tyr | Gly | Glu | Arg | Asp | Trp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Ala | Lys | Lys | Gly | Cys | Gln | Arg | Ile | Thr | Arg | Lys | Ser | Cys | Asn | Leu |
| | 50 | | | | 55 | | | | 60 | | | | | | |
| Thr | Val | Glu | Thr | Gly | Asn | Leu | Thr | Glu | Leu | Tyr | Tyr | Ala | Arg | Val | Thr |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ala | Val | Ser | Ala | Gly | Gly | Arg | Ser | Ala | Thr | Lys | Met | Thr | Asp | Arg | Phe |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ser | Ser | Leu | Gln | His | Thr | Thr | Leu | Lys | Pro | Pro | Asp | Val | Thr | Cys | Ile |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Lys | Val | Arg | Ser | Ile | Gln | Met | Ile | Val | His | Pro | Thr | Pro | Thr | Pro |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Ile | Arg | Ala | Gly | Asp | Gly | His | Arg | Leu | Thr | Leu | Glu | Asp | Ile | Phe | His |
| | 130 | | | | | 135 | | | | | 140 | | | | |

0972094.120100

Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
 145 150 155 160
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 165 170 175
 Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
 180 185 190
 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
 195 200 205
 Thr Trp Thr
 210

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 Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
 35 40 45
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
 50 55 60
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
 65 70 75 80
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
 85 90 95
 Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
 100 105 110
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
 115 120 125
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
 130 135 140
 Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
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 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
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 Thr Thr His Asp Glu Thr Val
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 20 25 30
 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
 85 90 95
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
 100 105 110
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
 130 135 140
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
 145 150 155 160
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
 165 170 175
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
 180 185 190
 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
 195 200 205
 Thr Arg Gln
 210

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